

SEQUENCE LISTING



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TECH CENTER 1600/2900

<110> Mahajan, Pramod B.
Zuo, Zhuang

<120> Poly ADP-Ribose Polymerase Gene and Its Uses

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<140> 09/236,995

<141> 1999-01-26

<150> 60/072,785

<151> 1998-01-27

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<170> PatentIn Ver. 2.1

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Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
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cgt ctt ggc aag atg gtt cag gcg tca cag ttc gac ggc ttc atg ccg 144

Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
 35 40 45

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gag aag ata cga aac tac gtt ggg agt gcc tca gct ggt aca agt tct 288
 Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
 85 90 95

aca gct gct cct cct gag aaa tgt aca att gag att gct cca tct gcc 336
 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
 100 105 110

cgt act tca tgt aga cga tgc agt gaa aag att aca aaa gga tcg gtc 384
 Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
 115 120 125

cgt ctt tca gct aag ctt gag agt gaa ggt ccc aag ggt ata cca tgg 432
 Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
 130 135 140

tat cat gcc aac tgt ttc ttt gag gta tcc ccg tct gca act gtt gag 480
 Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
 145 150 155 160

aag ttc tca ggc tgg gat act ttg tcc gat gag gat aag aga acc atg 528
 Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
 165 170 175

ctc gat ctt gtt aaa aaa gat gtt ggc aac aat gaa caa aat aag ggt 576
 Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly
 180 185 190

tcc aag cgc aag aaa agt gaa aat gat att gat agc tac aaa tcc gcc 624
 Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala
 195 200 205

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 Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln
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Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg	
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Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa	
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gra tgg gaa aag cat ata caa tgc amc ctt aaa cat gtt ctg acc tgn	1584
Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa	
515 520 525	
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His Xaa Val Cys Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp	
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Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala	
565 570 575	
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Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp	
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	675	680 685
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Leu Xaa Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu		
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	740	745 750
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Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys		
	755	760 765
gac atc acc ccg ctg gct cac gat agt gaa gat tac aag tta att gag		2352
Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu		
	770	775 780
cag tat ctc ctc aac aca cat gct cct act cac aag gac tgg tcg ctg		2400
Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu		
785	790	795 800
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805 810 815	
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Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His	
820 825 830	
ggt tca agg ttg acg aat ttt gtg gga att ctt agt caa ggg cta aga	2544
Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg	
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850 855 860	
ctc tac ttt gca gat cta gta agc aag agc gca caa tac tgt tat gtg	2640
Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Gln Tyr Cys Tyr Val	
865 870 875 880	
gat agg aat aat cct gta ggt ttg atg ctt ctt tct gag gtt gct tta	2688
Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu	
885 890 895	
gga gac atg tat gaa cta aag aaa gcc acg tcc atg gac aaa cct cca	2736
Gly Asp Met Tyr Glu Leu Lys Lys Ala Thr Ser Met Asp Lys Pro Pro	
900 905 910	
aga ggg aag cat tcg acc aag gga tta ggc aaa acc gtg cca ctg gag	2784
Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu	
915 920 925	
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Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro Cys Gly Lys	
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ccg gtg cca tca tca att agg agc tct gaa ctc atg tac aat gag tac	2880
Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr	
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Ile Val Tyr Asn Thr Ser Gln Val Lys Met Gln Phe Leu Leu Lys Val	
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 35 40 45
 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
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 130 135 140
 Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
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 Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
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 180 185 190
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 195 200 205
 Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln
 210 215 220
 Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu
 225 230 235 240
 Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu
 245 250 255
 Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn
 260 265 270
 Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala
 275 280 285
 Asp Gly Met Leu Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn
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 325 330 335

Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys
 340 345 350
 Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro
 355 360 365
 Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu
 370 375 380
 Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln
 385 390 395 400
 Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly
 405 410 415
 Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala
 420 425 430
 Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg
 435 440 445
 Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys
 450 455 460
 Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu
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 Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa
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 Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa
 515 520 525
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 565 570 575
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 580 585 590
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 595 600 605
 Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys
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 660 665 670
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 675 680 685
 Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu
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 35 40 45

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 Thr Ser Met Asp Lys Pro Pro Arg Gly Lys His Ser Thr Lys Gly Leu
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Ser	Ala	Gln	Tyr	Cys	Tyr	Val	Asp	Arg	Asn	Asn	Pro	Val	Gly	Leu	Met			
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Leu	Leu	Ser	Glu	Val	Ala	Leu	Gly	Asp	Met	Tyr	Glu	Leu	Lys	Lys	Ala			
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Thr	Ser	Met	Asp	Lys	Pro	Pro	Arg	Gly	Lys	His	Ser	Thr	Lys	Gly	Leu			
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Gly	Lys	Thr	Val	Pro	Leu	Glu	Ser	Glu	Phe	Val	Lys	Trp	Arg	Asp	Asp			
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Val	Val	Val	Pro	Cys	Gly	Lys	Pro	Val	Pro	Ser	Ser	Ile	Arg	Ser	Ser			
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Glu	Leu	Met	Tyr	Asn	Glu	Tyr	Ile	Val	Tyr	Asn	Thr	Ser	Gln	Val	Lys			
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